



SEQUENCE LISTING

<110> Walker, Ameae M.

<120> PROLACTIN ANTAGONISTS AND USES THEREOF

<130> Walker_2500_097US2

<140> 09/065,330

<141> 1998-04-23

<150> PCT/US97/01435

<151> 1997-01-30

<150> 08/594,809

<151> 1996-01-31

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (622)..(624)

<223> This is the codon for the substituted amino acids
of the mutated sequence.

<400> 1

```
aacatgaaca tcaaaggatc gccatggaaa gggtcctcc tgctgctgct ggtgtcaaac 60
ctgctgctgt gccagagcgt ggcccccttg cccatctgtc ccggcggggc tgcccgatgc 120
caggtgaccc ttcgagacct gtttgaccgc gccgtcgtcc tgtcccacta catccataac 180
ctctcctcag aaatgttcag cgaattcgat aaacggtata cccatggccg ggggttcatt 240
accaaggcca tcaacagctg ccacacttct tcccttgcca ccccgaaga caaggagcaa 300
gcccaacaga tgaatcaaaa agactttctg agcctgatag tcagcatatt gcgatcctgg 360
aatgagcctc tgtatcatct ggtcacggaa gtacgtggta tgcaagaagc cccggaggct 420
atctatcca aagctgtaga gattgaggag caaacaaaac ggcttctaga gggcatggag 480
ctgatagtca gccaggttca tcctgaaacc aaagaaaatg agatctaacc tgtctggtcg 540
ggacttccat cctgcagat ggctgatgaa gagtctcgcc tttctgctta ttataacctg 600
ctccactgcc tacgcaggga tnnncataaa atcgacaatt atctcaagct cctgaagtgc 660
cgaatcatcc acaacaacaa ctgctaagcc cacatccatt tcatctattt ctgagaaggt 720
ccttaatgat ccgttccatt gcaagcttct tttagttgta tctcttttga atccatgctt 780
gggtgtaaca ggtctcctct taaaaaataa aaactgactc gttagagaca tc 832
```

<210> 2
 <211> 228
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (208)
 <223> Site mutated codon where the normal codon coding
 for serine is modified preferably to encode for
 aspartate or glutamate, most preferably aspartate.

<400> 2
 Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu Leu
 1 5 10 15
 Leu Val Ser Asn Leu Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile
 20 25 30
 Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe
 35 40 45
 Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu
 50 55 60
 Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile
 65 70 75 80
 Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu
 85 90 95
 Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu
 100 105 110
 Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val
 115 120 125
 Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys
 130 135 140
 Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu Glu Gly Met Glu
 145 150 155 160
 Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr
 165 170 175
 Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser
 180 185 190

Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa
195 200 205

His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His
210 215 220

Asn Asn Asn Cys
225

<210> 3
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence
is a primer.

C
<400> 3
gcagggatga ccacaagggtt gac

23

<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence
is a primer.

<220>
<221> variation
<222> (12)
<223> This is a codon that can be replaced for nucleic
acid substitutes.

<400> 4
cgcaagggat gnacacaagg ttga

24

<210> 5
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence
is a primer.

<220>
<221> variation
<222> (12)
<223> This is a codon that can be replaced for nucleic
acid substitutes.

CI
<400> 5
acgcagggat gnkataaaat cg

22

<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence
is a primer.

<400> 6
cgtggccccc atatgttgcc catctg

26